

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/509,073A
Source: PT/10
Date Processed by STIC: 10/28/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/509,073A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics**
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 10/28/2005

PATENT APPLICATION: US/10/509,073A

TIME: 11:59:25

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10282005\J509073A.raw

4 <110> APPLICANT: TSUNEOKA, Makoto
 5 KIMURA, Hiroshi
 7 <120> TITLE OF INVENTION: Cancer-Associated Gene Mina53, Protein Mina53 and Monoclonal Antibody
 8 Thereof
 10 <130> FILE REFERENCE: 2004-1597A/WMC/00279
 12 <140> CURRENT APPLICATION NUMBER: 10/509,073A
 C--> 13 <141> CURRENT FILING DATE: 2004-10-12
 15 <160> NUMBER OF SEQ ID NOS: 3

*see items 2 and 4 on
 Error summary sheet*

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1395
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <400> SEQUENCE: 1
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 24 Met Pro Lys Lys Ala Lys Pro Thr Gly Ser Gly Lys Glu Glu Gly Pro Ala Pro
 25 5 10 15
 E--> 27 tgt aag cag atg aag tta gaa gca gct ggg ggg cct tca gct tta aac ttt gac 108
 28 108
 29 Cys Lys Gln Met Lys leu Glu Ala Ala Gly Gly Pro Ser Ala Leu Asn Phe Asp
 30 20 25 30 35
 E--> 32 agt ccc agt agt ctc ttt gaa agt tta atc tcg ccc atc aag aca gag act ttt 162
 33 162
 34 Ser Pro Ser Ser Leu Phe Glu Ser Leu Ile Ser Pro Ile Lys Thr Glu Thr Phe
 35 40 45 50
 E--> 37 ttc aag gaa ttc tgg gag cag aag ccc ctt ctc att cag aga gat gac cct gca
 38 216
 39 Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu Leu Ile Gln Arg Asp Asp Pro Ala
 40 55 60 65 70
 E--> 42 ctg gcc aca tac tat ggg tcc ctg ttc aag cta aca gat ctg aag agt ctg tgc
 43 270
 44 Leu Ala Thr Tyr Tyr Gly Ser Leu Phe Lys Leu Thr Asp Leu Lys Ser Leu Cys
 45 75 80 85 90
 E--> 47 agc cgg ggg atg tac tat gga aga gat gtg aat gtc tgc cgg tgt gtc aat ggg
 48 324
 49 Ser Arg Gly Met Tyr Tyr Gly Arg Asp Val Asn Val Cys Arg Cys Val Asn Gly
 50 95 100 105
 E--> 52 aag aag aag gtt tta aat aaa gat ggc aaa gca cac ttt ctt cag ctg aga aaa
 53 378
 54 Lys Lys Lys Val Leu Asn Lys Asp Gly Lys Ala His Phe Leu Gln Leu Arg Lys

*Does Not Comply
 corrected Diskette Needed*

*pp 1-7 insert hard
 return (see bottom
 of page)*

*see
 item 1
 on
 Error
 summary
 sheet*

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Input Set : A:\PTO.RJ.txt

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55      110      115      120      125
E--> 57 gat ttt gat cag aaa agg gca acg att cag ttt cac caa cct cag aga ttt aag
58 432
59 Asp Phe Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
60      130      135      140
E--> 62 gat gag ctt tgg agg atc cag gag aag ctg gaa tgt tac ttt ggc tcc ttg gtt
63 486
64 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser Leu Val
65 145      150      155      160
E--> 67 ggc tcg aat gtg tac ata act ccc gca gga tct cag ggc ctg ccg ccc cat tat
68 540
69 Gly Ser Asn Val Tyr Ile Thr Pro Ala Gly Ser Gln Gly Leu Pro Pro His Tyr
70      165      170      175      180
E--> 72 gat gat gtc gag gtt ttc atc ctg cag ctg gag gga gag aaa cac tgg cgc ctc
73 594
74 Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly Glu Lys His Trp Arg Leu
75      185      190      195
E--> 77 tac cac ccc act gtg ccc ctg gca cga gag tac agc gtg gag gcc gag gaa agg
78 648
79 Tyr His Pro Thr Val Pro Leu Ala Arg Glu Tyr Ser Val Glu Ala Glu Glu Arg
80      200      205      210      215
E--> 82 atc ggc agg ccg gtg cat gag ttt atg ctg aag ccg ggt gat ttg ttg tac ttt
83 702
84 Ile Gly Arg Pro Val His Glu Phe Met Leu Lys Pro Gly Asp Leu Leu Tyr Phe
85      220      225      230
E--> 87 ccc aga gga acc att cat caa gcg gac act cct gcg ggg ctg gcc cac tcg act
88 756
89 Pro Arg Gly Thr Ile His Gln Ala Asp Thr Pro Ala Gly Leu Ala His Ser Thr
90 235      240      245      250
E--> 92 cac gtg acc atc agc acc tac cag aac aat tca tgg gga gat ttc ctt ttg gat
93 810
94 His Val Thr Ile Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Phe Leu Leu Asp
95      255      260      265      270
E--> 97 acc atc tcg ggg ctt gta ttt gat act gca aag gaa gac gtg gag tta cgg acc
98 864
99 Thr Ile Ser Gly Leu Val Phe Asp Thr Ala Lys Glu Asp Val Glu Leu Arg Thr
100      275      280      285
E--> 102 ggc ata ccc cgg cag ctg ctc ctg gtg gaa tcc aca act gtt gct aca aga cga
103 918
104 Gly Ile Pro Arg Gln Leu Leu Leu Val Glu Ser Thr Thr Val Ala Thr Arg Arg
105      290      295      300      305
E--> 107 tta agt ggc ttc ctg agg aca ctt gca gac cgg ctg gag ggc acc aaa gaa ctg
108 972
109 Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Arg Leu Glu Gly Thr Lys Glu Leu
110      310      315      320
E--> 112 ctt tcc tca gac atg aag aag gat ttt att atg cac aga ctc ccc cct tac tct
113 1026
114 Leu Ser Ser Asp Met Lys Lys Asp Phe Ile Met His Arg Leu Pro Pro Tyr Ser
115 325      330      335      340

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same
enr

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Input Set : A:\PTO.RJ.txt

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E--> 117 gcg gga gat ggg gca gag ctg tca aca cca ggt gga aag tta ccg agg ctg gac
      118 1080
      119 Ala Gly Asp Gly Ala Glu Leu Ser Thr Pro Gly Gly Lys Leu Pro Arg Leu Asp
      120          345          350          355          360
E--> 122 agt gta gtg aga ctg cag ttt aaa gac cac att gtc ctc aca gta ctg ccg gat
      123 1134
      124 Ser Val Val Arg Leu gln Phe Lys Asp His Ile Val Leu Thr Val Leu Pro Asp
      125          365          370          375
E--> 127 caa gat caa tct gat gaa gct caa gaa aag atg gtg tac atc tat cat tcc tta
      128 1188
      129 Gln Asp Gln Ser Asp Glu Ala Gln Glu Lys Met Val Tyr Ile Tyr His Ser Leu
      130          380          385          390          395
E--> 132 aag aat agt aga gag aca cac atg atg gga aat gag gag gaa aca gag ttt cat same
      133 1242
      134 Lys Asn Ser Arg Glu Thr His Met Met Gly Asn Glu Glu Glu Thr Glu Phe His
      135          400          405          410
E--> 137 gga ctt cgc ttc cct ttg tca cat ttg gat gca ctg aag caa att tgg aat agt
      138 1296
      139 Gly Leu Arg Phe Pro Leu Ser His Leu Asp Ala Leu Lys Gln Ile Trp Asn Ser
      140 415          420          425          430
E--> 142 cca gct att tct gtc aag gac ctg aaa ctt act aca gat gag gaa aag gaa agc
      143 1350
      144 Pro Ala Ile Ser Val Lys Asp Leu Lys Leu Thr Thr Asp Glu Glu Lys Glu Ser
      145          435          440          445          450
E--> 147 ctg gta tta tcc ctc tgg aca gaa tgt tta att caa gta gtc tag
      148 1395
      149 Leu Val Leu Ser Leu Trp Thr Glu Cys Leu Ile Gln Val Val
      150          455          460
      152 <210> SEQ ID NO: 2
      153 <211> LENGTH: 1398
      154 <212> TYPE: DNA
      155 <213> ORGANISM: Mus musculus
      157 <400> SEQUENCE: 2
      158 atg cca aag aaa gtg cag ccc aca ggg gat gag aac gaa gaa gag tct gtt cct 54
      159 Met Pro Lys Lys Val Gln Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser Val Pro
      160          5          10          15
E--> 162 tgc aag cgg gtg aag gag gag ctg cct gaa acg ctt tct gta tta aac ttt gac
      163 108
      164 Cys Lys Arg Val Lys Glu Glu Leu Pro Glu Thr Leu Ser Val Leu Asn Phe Asp same
      165          20          25          30          35
E--> 167 agc ccc agt agt ttc ttc gaa agt tta atc tca ccc atc aaa gta gag act ttt
      168 162
      169 Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro Ile Lys Val Glu Thr Phe
      170          40          45          50
E--> 172 ttc aag gaa ttc tgg gaa caa aag ccc ctt ctc att cag agg gat gac cct gta
      173 216
      174 Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu Leu Ile Gln Arg Asp Asp Pro Val
      175 55          60          65          70
E--> 177 ctg gcc aaa tat tac cag tct ctg ttc agc ctc tca gat ctg aag aga ctc tgc

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178 270
179 Leu Ala Lys Tyr Tyr Gln Ser Leu Phe Ser Leu Ser Asp Leu Lys Arg Leu Cys
180      75      80      85      90
E--> 182 aag aaa gga gtg tac tat gga aga gac gtg aat gtc tgc cgg agc atc agt ggg
183 324
184 Lys Lys Gly Val Tyr Tyr Gly Arg Asp Val Asn Val Cys Arg Ser Ile Ser Gly
185      95      100      105
E--> 187 aag aag aag gtt tta aat aag gat ggc aga gca cat ttt ctt cag ctg aga aaa
188 378
189 Lys Lys Lys Val Leu Asn Lys Asp Gly Arg Ala His Phe Leu Gln Leu Arg Lys
190      110      115      120      125
E--> 192 gat ttt gat cag aag agg gca aca att cag ttt cac caa cct cag aga tat aag
193 432
194 Asp Phe Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Tyr Lys
195      130      135      140
E--> 197 gat gag ctg tgg cgg atc cag gaa aag ctg gaa tgt tac ttt ggg tcc tta gta
198 486
199 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser Leu Val
200 145      150      155      160
E--> 202 ggc tcg aat gtg tac atg act cct gca gga tct cag ggc ctc cct cca cat tat
203 540
204 Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu Pro Pro His Tyr
205      165      170      175      180
E--> 207 gat gat gtt gag gtt ttt atc ctg cag ctg gag gga acg aaa cac tgg cgc ctg
208 594
209 Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly Thr Lys His Trp Arg Leu
210      185      190      195
E--> 212 tac tcc cca act gtg ccc ctg gca cac gag tac agt gtg gaa tct gag gac cgg
213 648
214 Tyr Ser Pro Thr Val Pro Leu Ala His Glu Tyr Ser Val Glu Ser Glu Asp Arg
215      200      205      210      215
E--> 217 atc ggc aca ccg aca cac gac ttc ctg ctg aag cct gga gat ttg ttg tac ttt
218 702
219 Ile Gly Thr Pro Thr His Asp Phe Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe
220      220      225      230
E--> 222 ccc aga ggg acc att cat cag gca gaa act cct tca ggc ctg gcc tac tct att
223 756
224 Pro Arg Gly Thr Ile His Gln Ala Glu Thr Pro Ser Gly Leu Ala Tyr Ser Ile
225 235      240      245      250
E--> 227 cac ctg act att agc acc tac cag aac aat tca tgg gga gac tgc ctt ttg gat
228 810
229 His Leu Thr Ile Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Cys Leu Leu Asp
230      255      260      265      270
E--> 232 tcc att tcg ggg ttc gta ttt gac att gca aag gaa gat gtg gca tta agg agt
233 864
234 Ser Ile Ser Gly Phe Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Ser
235      275      280      285
E--> 237 gga atg ccc cgg cgg atg ctc ctg aat gtg gaa acc cca gct gat gta aca agg
238 918

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same

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239 Gly Met Pro Arg Arg Met Leu Leu Asn Val Glu Thr Pro Ala Asp Val Thr Arg
240      290      295      300      305
E--> 242 aag ttg agt ggc ttt ctg agg act ctt gca gac cag ctc gag ggc aga gaa gag
243      972
244 Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu Gly Arg Glu Glu
245      310      315      320
E--> 247 ctg ctg tca tca gat atg aag aag gac ttc gtc aag cac aga ctc cct cct ttc
248     1026
249 Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Lys His Arg Leu Pro Pro Phe
250     325      330      335      340
E--> 252 ttc gag gga aat gga acg gag acg atg gac cca ggt aaa cag ttg cca agg ttg
253     1080
254 Phe Glu Gly Asn Gly Thr Glu Thr Met Asp Pro Gly Lys Gln Leu Pro Arg Leu
255      345      350      355      360
E--> 257 gac aac ata ata aga ctg cag ttc aaa gat cac att gtc ctc aca gta ggg cca
258     1134
259 Asp Asn Ile Ile Arg Leu Gln Phe Lys Asp His Ile Val Leu Thr Val Gly Pro
260      365      370      375
E--> 262 gat aag aat cca ttt gat gaa gct caa caa aag gtg gtt tac atc tat cat tct
263     1188
264 Asp Lys Asn Pro Phe Asp Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser
265      380      385      390      395
E--> 267 ctg aag aat gtg agg cag atg cac atg ata gga gaa gag gag gaa tcc gag att
268     1242
269 Leu Lys Asn Val Arg Gln Met His Met Ile Gly Glu Glu Glu Glu Ser Glu Ile
270      400      405      410
E--> 272 ttc ggt ctt cgc ttt cct tta tca cat gtg gat gct ctg aag caa atc tgg tgc
273     1296
274 Phe Gly Leu Arg Phe Pro Leu Ser His Val Asp Ala Leu Lys Gln Ile Trp Cys
275     415      420      425      430
E--> 277 ggg tca cca att cgt gtt aag gaa ctg aaa ctt gac aca gat gaa gaa aag gag
278     1350
279 Gly Ser Pro Ile Arg Val Lys Glu Leu Lys Leu Asp Thr Asp Glu Glu Lys Glu
280      435      440      445      450
E--> 282 aac ctg gca ctg tct ctc tgg tgc gag tct tta atc caa gta ctc tag
283     1398
284 Asn Leu Ala Leu Ser Leu Trp Ser Glu Ser Leu Ile Gln Val Leu
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289 <211> LENGTH: 1398
290 <212> TYPE: DNA
291 <213> ORGANISM: Rattus norvegicus
293 <400> SEQUENCE: 3
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296 Met Pro Lys Lys Val Lys Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser Val Pro
297      5      10      15
E--> 299 tgc aag cag gtg aaa gag gag cta cct aat acg ctt tct gta tta aac ttt gac
300     108
301 Cys Lys Gln Val Lys Glu Glu Leu Pro Asn Thr Leu Ser Val Leu Asn Phe Asp

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      302      20      25      30      35
E--> 304 agc ccc agt agt ttc ttt gaa agt tta ata tca ccc atc aaa gta gag aca ttt
      305 162
      306 Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro Ile Lys Val Glu Thr Phe
      307      40      45      50
E--> 309 ttc aag gaa ttc tgg gaa cag aag ccc ctt ctc att cag aga gat gac cct tgc
      310 216
      311 Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu Leu Ile Gln Arg Asp Asp Pro Ser
      312 55      60      65      70
E--> 314 ctg gcc gca tat tac cag tct ctg ttc agc ctc tca gat ctg agg agt ctc tgc
      315 270
      316 Leu Ala Ala Tyr Tyr Gln Ser Leu Phe Ser Leu Ser Asp Leu Arg Ser Leu Cys
      317      75      80      85      90
E--> 319 agc caa ggg ctg tac tat gga aga gat gtc aat gtc tgc cgg tgc atc ggt ggg
      320 324
      321 Ser Gln Gly Leu Tyr Tyr Gly Arg Asp Val Asn Val Cys Arg Cys Ile Gly Gly
      322      95      100      105
E--> 324 aag aag aag gtt tta aat aag gat ggc aaa gca cag ttt ctt cag ctg aga aaa
      325 378
      326 Lys Lys Lys Val Leu Asn Lys Asp Gly Lys Ala Gln Phe Leu Gln Leu Arg Lys
      327 110      115      120      125
E--> 329 gat ttt gat cag aag agg gca aca att cag ttt cat cag cca cag aga ttt aag
      330 432
      331 Asp Phe Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
      332      130      135      140
E--> 334 gat gag ctc tgg agg atc cag gaa aag ctg gaa tgt tac ttt ggc tcc tta gta
      335 486
      336 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser Leu Val
      337 145      150      155      160
E--> 339 ggc tca aat gtg tac atg act ccc gca gga tct cag ggc ctt cct cca cat tac
      340 540
      341 Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu Pro Pro His Tyr
      342      165      170      175      180
E--> 344 gac gat gtt gag gtt ttt atc ctg cag ctg gag gga agg aaa cgt tgg cgc ctg
      345 594
      346 Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly Arg Lys Arg Trp Arg Leu
      347      185      190      195
E--> 349 tac tcc cca act gtg ccc ctg gcg cgt gag tac agt gtg gag cct gag gac cgg
      350 648
      351 Tyr Ser Pro Thr Val Pro Leu Ala Arg Glu Tyr Ser Val Glu Pro Glu Asp Arg
      352      200      205      210      215
E--> 354 att ggc aca cca aca cat gac ttc ctg ctg aag cct ggc gat ttg ttg tac ttc
      355 702
      356 Ile Gly Thr Pro Thr His Asp Phe Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe
      357      220      225      230
E--> 359 ccc aga ggg acc att cac cag gca gaa act cct tca ggc ctg gcc cac tct att
      360 756
      361 Pro Arg Gly Thr Ile His Gln Ala Glu Thr Pro Ser Gly Leu Ala His Ser Ile
      362 235      240      245      250

```

same

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E--> 364 cac ctg act att agc acc tac cag aac aat tca tgg gga gat tac ctt ttg gac
      365 810
      366 His Leu Thr Ile Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Tyr Leu Leu Asp
      367 255 260 265 270
E--> 369 tcc att tcg ggg ctt gta ttt gac att gca aag gaa gat gtg gca tta agg act
      370 864
      371 Ser Ile Ser Gly Leu Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Thr
      372 275 280 285
E--> 374 gga atg ccc agg cgg atg ctc atg aat gtg gaa acc cca gct gac gta aca agg
      375 918
      376 Gly Met Pro Arg Arg Met Leu Met Asn Val Glu Thr Pro Ala Asp Val Thr Arg
      377 290 295 300 305
E--> 379 aag ttg agt ggc ttt ctg agg act ctg gca gac cag ctc gag ggc aga aaa gaa
      380 972
      381 Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu Gly Arg Lys Glu
      382 310 315 320
E--> 384 ctg ctc tca tca gat atg aag aag gac ttc gtc atg cac aga ctt ccc cct ttc
      385 1026
      386 Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Met His Arg Leu Pro Pro Phe
      387 325 330 335 340
E--> 389 tgt gtg gga aat gga aca gag tca atg aac cca ggt gga aag ttg cca agg ttg
      390 1080
      391 Cys Val Gly Asn Gly Thr Glu Ser Met Asn Pro Gly Gly Lys Leu Pro Arg Leu
      392 345 350 355 360
E--> 394 aac agc ata gta aga ctg cag ttt aaa gac cac att gtc ctc aca gta ggg ccc
      395 1134
      396 Asn Ser Ile Val Arg Leu Gln Phe Lys Asp His Ile Val Leu Thr Val Gly Pro
      397 365 370 375
E--> 399 gat cag aat caa tct gat gaa gct caa caa aag gtg gtt tac atc tac cat tct
      400 1188
      401 Asp Gln Asn Gln Ser Asp Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser
      402 380 385 390 395
E--> 404 cta aag aat gag aga cag acg cac atg atg ggg aaa gag gtg gaa aca gag att
      405 1242
      406 Leu Lys Asn Glu Arg Gln Thr His Met Met Gly Lys Glu Val Glu Thr Glu Ile
      407 400 405 410
E--> 409 tat gga ctt cgc ttt cct tta tcc tat gtg gac gct ctg aag caa atc tgg tgc
      410 1296
      411 Tyr Gly Leu Arg Phe Pro Leu Ser Tyr Val Asp Ala Leu Lys Gln Ile Trp Cys
      412 415 420 425 430
E--> 414 ggg tca cca gtt cgt gtt aag gac ctg aaa ctt ggc aca gat gaa gag aag gag
      415 1350
      416 Gly Ser Pro Val Arg Val Lys Asp Leu Lys Leu Gly Thr Asp Glu Glu Lys Glu
      417 435 440 445 450
E--> 419 aac ctg gca gtg tct ctc tgg aca gag tgt cta gtc cac gtg ctc tag
      420 1398
      421 Asn Leu Ala Val Ser Leu Trp Thr Glu Cys Leu Val His Val Leu
      422 455 460 465

```

same

VERIFICATION SUMMARY

DATE: 10/28/2005

PATENT APPLICATION: US/10/509,073A

TIME: 11:59:26

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10282005\J509073A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:108 SEQ:1
L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:162 SEQ:1
L:37 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:216 SEQ:1
L:42 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:270 SEQ:1
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:324 SEQ:1
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:378 SEQ:1
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:432 SEQ:1
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:486 SEQ:1
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:1
L:72 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:594 SEQ:1
L:77 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:648 SEQ:1
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:702 SEQ:1
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:756 SEQ:1
L:92 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:810 SEQ:1
L:97 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:864 SEQ:1
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:918 SEQ:1
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:972 SEQ:1
L:112 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1026 SEQ:1
L:117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:1
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1134 SEQ:1
L:127 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1188 SEQ:1
L:132 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1242 SEQ:1
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1296 SEQ:1
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1350 SEQ:1
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1395 SEQ:1
L:162 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:108 SEQ:2
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:162 SEQ:2
L:172 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:216 SEQ:2
L:177 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:270 SEQ:2
L:182 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:324 SEQ:2
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:378 SEQ:2
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:432 SEQ:2
L:197 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:486 SEQ:2
L:202 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:2
L:207 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:594 SEQ:2
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:648 SEQ:2
L:217 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:702 SEQ:2
L:222 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:756 SEQ:2
L:227 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:810 SEQ:2
L:232 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:864 SEQ:2
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:918 SEQ:2
L:242 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:972 SEQ:2
L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1026 SEQ:2
L:252 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:2
L:257 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1134 SEQ:2
L:262 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1188 SEQ:2
L:267 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1242 SEQ:2

VERIFICATION SUMMARY

DATE: 10/28/2005

PATENT APPLICATION: US/10/509,073A

TIME: 11:59:26

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10282005\J509073A.raw

L:272 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1296 SEQ:2
L:277 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1350 SEQ:2
L:282 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1398 SEQ:2
L:299 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:108 SEQ:3
L:304 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:162 SEQ:3
L:309 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:216 SEQ:3
L:314 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:270 SEQ:3
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:324 SEQ:3
L:324 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:378 SEQ:3
L:329 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:432 SEQ:3
L:334 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:486 SEQ:3
L:339 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:3
L:344 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:594 SEQ:3
L:349 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:648 SEQ:3
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:702 SEQ:3
L:359 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:756 SEQ:3
L:364 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:810 SEQ:3
L:369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:864 SEQ:3
L:374 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:918 SEQ:3
L:379 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:972 SEQ:3
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1026 SEQ:3
L:389 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:3
L:394 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1134 SEQ:3
L:399 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1188 SEQ:3
L:404 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1242 SEQ:3
L:409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1296 SEQ:3
L:414 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1350 SEQ:3
L:419 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1398 SEQ:3